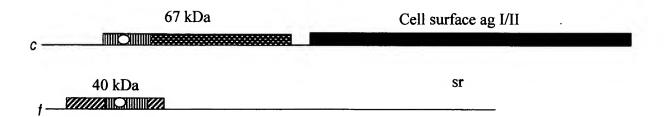
# FIGURE 1A

	10	20 I	30	40	50	60		
serotype f	MNQKIVVISSFYM	•		RIDINHQAQE				
serotype c			<u>MK</u>	RIDINHQAQR	FSIRKYAFGA	ASVLIG		
	70	80	90	100	110	120		
serotype f	CVFFLGTQNVSAQ	 EQGTQLPASE	 NAVVNVAENSV	 /AISQAVADKA	ATQTTLTETE	QVEVEE		
serotype c	CVFFLGTQNVSAQ							
	130 I	140 I	150 I	160 I	170 I	180		
serotype f	KESKVNAPALNVD							
serotype c	KENKVNAPALNVD	DKGAKSKEDVI	NPTVSKTASEV	EASAVTATDT	KNSNPQVNVE	ETDSNEK		
	190	200	210	220	230	240		
serotype f	DENKMVTSAPAKE		RENLMOROAKA	VSIPSQGNYV	FQETTP <u>VKN</u>	ASMSSP		
serotype c	DENKMVTSAPAKE			VSIPSQGNYV	FQETTP <u>VKN</u>	ASMSSP		
	250	260	270	280	290	300		
serotype f	TOFNFDKGDKVFY TEFNEDK*****							
serotype c	<b>TOFNFDK</b> GDKVFY							
	310 	320 	330 	340 I	350 I	360 I		
serotype f	TYHFTKQQSLK	MKLN		CLVRPNSRF1		r		
serotype c	TYHFTKQADV <u>KNE</u>	AKLSSPTOFS	FYNGDHVFYDK	VLEADGHOWI	SYVSYSGIRE	RYVVIGK		
	370 	380 I	390 I	400 	410 	420 		
serotype f serotype c	LTTQPSPIETKVS	GTIAIQNKTA	OOFDVIISNVS	STOGIKEVLV	PVWSEONGO	ONWYO		
	430	440	450	460	470	480		
serotype f				l	i			
serotype c	ATKOGEGVYKVTV	KVSDHKNNSG	NYDIHLYYRLS	TGELKVVGGF	(TTEVEAPKP)	/ETTGII		
	490	500	510	520	530	540		
serotype f		I	 	l	·	l		
serotype c	SIANKSS <u>OGFDVL</u>	ITNASSTOGI	KEVLVPVWSEC	ONGODDIIWYO	ATKOGEGVYE	KVTVKVS		
	550 I	560 I	570 I	580 I	590 	600 I		
serotype f serotype c	<u>DHKNDSGNYDIHLYYRLSTGELKVVGGKTTTVEAP</u> NRVNLPAQGTYVFTNKVE <u>VKNEART</u>							
	610	620	630	640				
serotype f	· I	I 	i	 				
serotype c	<u>SSPTOFTFNKGESIYYDSILNADGHQWISYRSYSGIRRY</u> IIID							

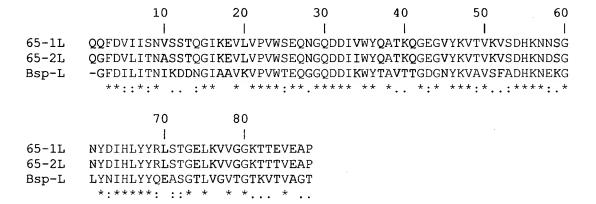
# FIGURE 1B

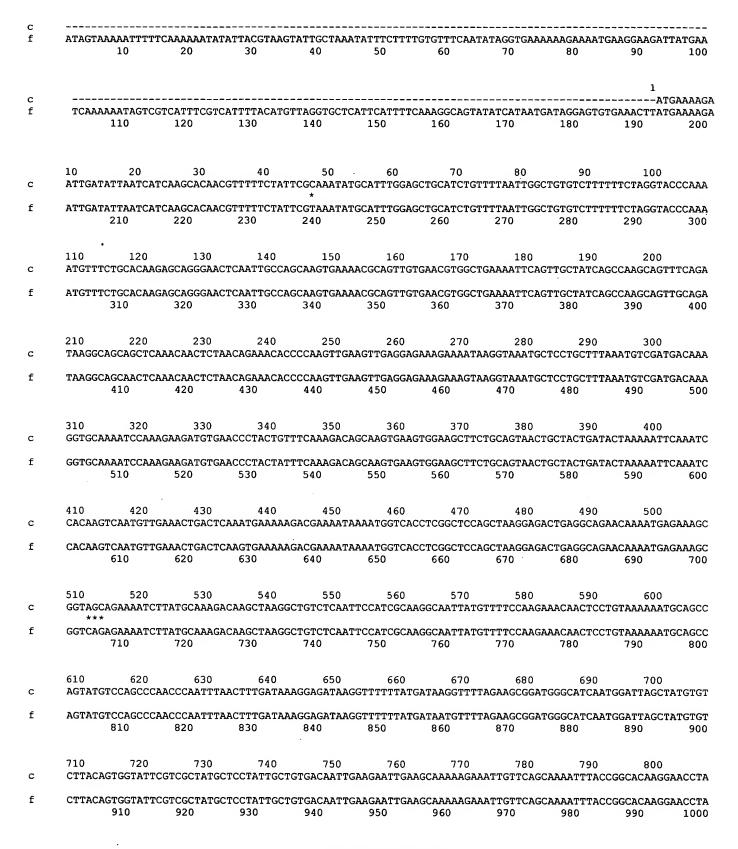


### FIGURE 2A

	10	20	30	40
	1	1	1	1
65-1s	VKNAASMSSPT	QFNFDKGDK\	/FYDKVLEADO	GHQWISYVSYSGIRRY
40-1s	VKNAASMSSPT	QFNFDKGDK\	/FYDNVLEADO	GHQWISY <b>V</b> SY <b>S</b> GIRRY
65-2s	VKNEAKLSSPI	QFSFYNGDHV	/FYDKVLEAD	GHQWISY <b>V</b> SY <b>S</b> GIRRY
65-3s	VKNEARTSSPI	QFTFNKGES	YYDSILNADO	GHQWISYRSYSGIRRY
Bsp-2s	VKNEAKVASPI	QFTLDKGDR	FYDQILTIE	GNQWLSYKSFNGVRRF
Bsp-3s	KEAKISSQT	QFTLEKGDK	NYDQVLTADO	GYQWISYKSYSGVRRY
Bsp-4s	VKSQPKVSSPV	EFNFQKGEK	HYDQVL <b>VV</b> D0	GHQWISYKSYSGIRRY
Bsp-1s	VKNTPSKSAPV	AFYAKKGDK	/FYDQVFNKDI	NVKWISYKSFCGVRRY
	:: .	* :*:	**.:: :	. :*:** *: *:**:
SH3b				DWADITYGSGQRGY
	* * ***	****	*	* * * *

### FIGURE 2B





С	810 820 TCACTTTACTAAACAA		840 850 GAAGCTAAACTGTC	860 TAGTCCGACCO	870 CAATTCTCGTT	880 TTACAACGGA	890 GATCAÇGTTI	900 TTTATGATAA	AGGTT
f	TCACTTTACTAAACA_	GCAGAGCTTAAAAAT 1020 1030	GAAGCTAAACTGTC 1040	TAGTCCGACCC 1050	•	TTACAACGGA 1070	GATCACGTTT 1080	TTTATGATAA 1090	AGGTT 1100
С	910 920 TTAGAAGCGGATGGGC		40 950 ATGTGTCCTACAGT	960 GGTATCCGTCC	970 GTTATGTTGTT	980 ATTGGAAAGC	990 TTACGACACA	1000 ACCCTCTCCA	ATTG
f	T <u>TAG</u> AAGCGGATGGAC 1110	ATCAATGGATTAGCT 1120 1130	ATGTGTCCTACAGT 1140	GGTATCCGTCC 1150		ATTGGAAAGC 1170	TTACGACACA 1180	ACCCTCTCCA 1190	ATTG 1200
С	1010 1020 AAACTAAAGTATCAGG		040 1050 AAATAAAACGGCTC	1060 AACAATTCGAT	1070 FGTTATCATTT	1080 CTAATGTTTC	1090 CAGCACTCAA	1100 AGGCATAAAA	GAGGT
f	AAACTAAAGTATCAGG 1210	TACTATTGTCATCCA	AAATAAAACGGCTC 1240	AACAATTCGAT 1250		* CTAATGCTTC 1270	* * AAGCAATCAA 1280	AGGCATAAAA 1290	SAGGT 1300
С	1110 1120 ATTAGTGCCGGTTTGG		140 1150 CAGGATGACATTGT	1160 CTGGTATCAAC	1170 GCAACTAAACAA **	1180 AGGCGAAGGC	1190 GTTTATAAGG	1200 STGACCGTTA	AGGTC
f	ATTAGTGCCAGTTTGG	TCAGAGCAAAACGGG 1320 1330	CAGGATGACATTGT 1340	CTGGTATCAAC 1350			GTTTATAAGG 1380	STGACCGTTAA 1390	AGGTC 1400
С	1210 1220 AGTGACCATAAAAATA	ACAGTGGTAACTATG	240 1250 ACATTCACCTTTAT	1260 TATCGCCTTTC		1280 TTAAAGGTTG		1300 AGACAACTGAG	GTGG
f	AGTGACCATAAAAATA				ATAATGGTGAA(			CAATGACTGAG	GTGG. 1500
С	1310 1320 AAGCACCGAAGCCTGTA	· · · · · · · · · · · · · · · · · · ·	340 1350 CATTAGCATTGCCA	1360 ATAAGAGCAG(	1370 CCAAGGATTTG	1380 ATGTTTTGAT	1390 TACTAATGCT	1400 TCCAGCACTO	CAAGG
f	** AAGCACCAGAGCCTGT	AGAAACAACAGGTAT 1520 1530	CATTAGCATTGCCA 1540	ATAAGAGCAGO 1550		ATGTTTTGAT 1570	TACTAATGCT 1580	TTCCAGCACTO	* CAAGA 1600
С						1480	1400		
	1410 1420 CATAAAAGAGGTATTAG		440 1450 GAACAAAACGGACA	1460 GGACGATATT	1470 ATTTGGTATCA		1490 CAAGGCGAAG	1500 GCGTTTATA	AGGTG
f	CATAAAAGAGGTATTA(  * CATAAAAGAGGTTTTA(	GTGCCAGTTTGGTCA *	GAACAAAACGGACA	GGACGATATTA	atttggtatca/ atttggtatca/	AGCAACTAAA	CAAGGCGAAG	GCGTTTATA	
	CATAAAAGAGGTATTA(  * CATAAAAGAGGTTTTA(	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630	GAACAAAACGGACA GAACAAAACGGACA 1640 540 1550	GGACGATATTA GGACGATATTA 1650 1560	ATTTGGTATCA/ATTTGGTATCA/ATTGGTATCA/ATTGGCATTGGCCTT	AGCAACTAAA AGCAACTAAA 1670 1580 ICAACTGGTG	CAAGGCGAAG CAAGGCGAAG 1680 1590	GGCGTTTATAA GGCGTTTATAA 1690	AGGTG 1700
f	CATAAAAGAGGTATTAA  CATAAAAGAGGTTTTAA 1610  1510 1520 ACCGTTAAGGTCAGTG	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630  1530 1 ACCATAAAAATGACA	GAACAAAACGGACA GAACAAAACGGACA 1640 540 1550 GTGGTAACTATGAC	GGACGATATTA GGACGATATTA 1650 1560 ATTCACCTTTA	ATTTGGTATCAL ATTTGGTATCAL 1660  1570 ATTATCGCCTT	AGCAACTAAA AGCAACTAAA 1670 1580 TCAACTGGTG	CAAGGCGAAG CAAGGCGAAG 1680 1590 GAATTAAAGGT	GGCGTTTATAA GGCGTTTATAA 1690 · 1600 TGTTGGAGGA	AGGTG 1700
f C	CATAAAAGAGGTATTAG  * CATAAAAGAGGTTTTAG 1610  1510 1520 ACCGTTAAGGTCAGTGG * GCCGTTAAGGTCAGTGGT1710  1610  1620	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630  1530 1 ACCATAAAAATGACA ACCATAAAAATGACA 1720 1730	GAACAAAACGGACA  GAACAAAACGGACA  1640  540  1550 GTGGTAACTATGAC  4 GTGGTAACTATAAC  1740  640  1650	GGACGATATTA 1650  1560 ATTCACCTTTA 1750  1660	ATTTGGTATCAN ATTTGGTATCAN 1660  1570 ATTATCGCCTT 1760  1670	AGCAACTAAA AGCAACTAAA 1670 1580 TCAACTGGTG *** GTAACTGGTG	CAAGGCGAAG 1680 1590 CAATTAAAGGT CAATTAAAGGT 1780	GGCGTTTATAP 1690 1600 TGTTGGAGGP 1790	AGGTG 1700 AAAGA AAAGA 1800
f c f	CATAAAAGAGGTATTAC  * CATAAAAGAGGTTTTAC 1610  1510 1520 ACCGTTAAGGTCAGTGC * GCCGTTAAGGTCAGTGC 1710 .  1610 1620 CAACGACAGTAGAAGCC CAACGACAGTAGAAGCC	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630  1530 1 ACCATAAAAATGACA ACCATAAAAAATGACA 1720 1730  1630 1 CCCTAATAGAGTCAA	GAACAAAACGGACA GAACAAAACGGACA 1640  540 1550 GTGGTAACTATGAC * * *GTGGTAACTATAAC 1740  640 1650 TCTTCCAGCACAAG	GGACGATATTA 1650  1560 ATTCACCTTTA 1750  1660 GAACTTATGTTA	ATTTGGTATCAL ATTTGGTATCAL 1660  1570 ATTATCGCCTTC 1760  1670 TTTCACTAATAL	AGCAACTAAA AGCAACTAAA 1670 1580 TCAACTGGTG ** STAACTGGTG 1770 1680 AAGTTGAGGT	CAAGGCGAAG CAAGGCGAAG 1680 1590 CAATTAAAGGT CAATTAAAGGT 1780	GGCGTTTATAP GGCGTTTATAP 1690  1600 TGTTGGAGGP TGTTGGAGGP 1790  1700 GGCCAGAACAT	AGGTG 1700 AAAGA AAAGA 1800
f c f	CATAAAAGAGGTATTAC  * CATAAAAGAGGTTTTAC 1610  1510 1520 ACCGTTAAGGTCAGTGC * GCCGTTAAGGTCAGTGC 1710 .  1610 1620 CAACGACAGTAGAAGCC CAACGACAGTAGAAGCC	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630  1530 1 ACCATAAAAAATGACA ACCATAAAAAATGACA 1720 1730  1630 1 CCCTAATAGAGTCAA * CCCTAATAGAGTCAA 1820 1830	GAACAAAACGGACA  GAACAAAACGGACA  1640  540  1550 GTGGTAACTATGAC  *  GTGGTAACTATAAC 1740  640  1650 TCTTCCAGCACAAG 1840  740  1750	GGACGATATTA 1650  1560 ATTCACCTTTA 1750  1660 GAACTTATGTT 1850	ATTTGGTATCAL ATTTGGTATCAL 1660  1570 ATTATCGCCTT 1760  1670 ATTCACTAATAL 1860  1770	AGCAACTAAA AGCAACTAAA 1670 1580 FCAACTGGTG ** GTAACTGGTG 1770 1680 AAGTTGAGGT AAGTTGAGGT	CAAGGCGAAG  CAAGGCGAAG  1680  1590  CAATTAAAGGT  1780  1690  TAAAAAATGAG  TAAAAATGAG  1880	GGCGTTTATAF 1690  1600 TGTTGGAGGF 1790  1700 GGCCAGAACAT 1890	AGGTG 1700 AAAGA AAAGA 1800 CCTAG CCTAG
f c f	CATAAAAGAGGTATTAC  CATAAAAGAGGTATTAC  1610  1510 1520 ACCGTTAAGGTCAGTG  * GCCGTTAAGGTCAGTG 1710  1610 1620 CAACGACAGTAGAAGC CAACGACAGTAGAAGC 1810  1710 1720 TCCAACTCAGTTTACC TCCAACTCAGTTTACC	GTGCCAGTTTGGTCA  * GTGCCGGTTTGGTCA 1620 1630  1530 1 ACCATAAAAAATGACA 1720 1730  1630 1 CCCTAATAGAGTCAA * CCCTAATAGAGTCAA 1820 1830  1730 1 TTTAATAAAAGGAGAA	GAACAAAACGGACA GAACAAAACGGACA 1640  540 1550 GTGGTAACTATGAC * GTGGTAACTATAAC 1740  640 1650 TCTTCCAGCACAAG 1840  740 1750 AGTATTACTATGA	GGACGATATTA 1650  1560 ATTCACCTTTA 1750  1660 GAACTTATGTT 1850  1760 CAGTATCTTGA	ATTTGGTATCAN ATTTGGTATCAN 1660  1570 ATTATCGCCTT 1760  1670 FTTCACTAATAN 1860  1770 AATGCTGATGGN	AGCAACTAAA AGCAACTAAA AGCAACTAAA AGCAACTGGTG ** GTAACTGGTG AAGTTGAGGT AAGTTGAGGT AAGTTGAGGT AAGTTGAGGT AAGTTGAGGT AAGTTGAGGT	CAAGGCGAAG  CAAGGCGAAG  1680  1590 CAATTAAAGGT  1780  1690 CTAAAAATGAG  1880  1790 CATTAGCTATC	GCCGTTTATAP GCCGTTTATAP 1690  1600 TTGTTGGAGGP 1790  1700 GCCCAGAACAT 1890  1800 CGTTCCTACAG	AGGTG 1700 AAAGA 1800 CCTAG 1900

FIGURE 3, CTD.

ATTCGTCGTTATATTATCATTGGTTGA 2010 2020

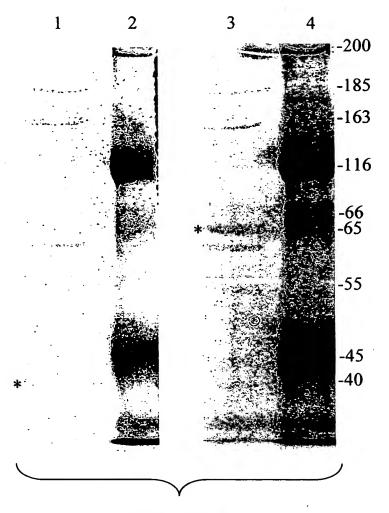
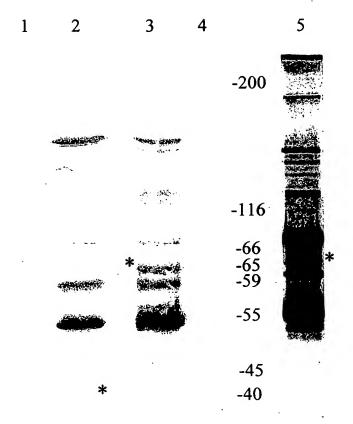
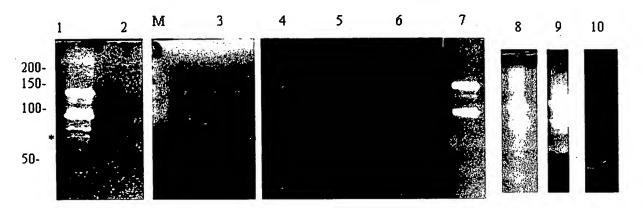


FIGURE 4





### **Enzyme source**

OMZ175 peptidoglycan:

Lane 1 - A32-2

Lane 2 - OMZ175

A32-2 peptidoglycan: Lane 3 - A32-2

Lane 4 - NG8

Lane 5 - SrtA-

Lane 6- OMZ175

Lane 7-UA159

### **Enzyme source**

S.sobrinus peptidoglycan: Lane 8 - A32-2

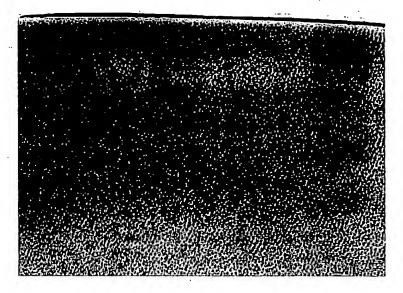
S. gordomi peptidoglycan: Lane 9 - A32-2

S. oralis peptidoglycan: Lane 10 - A32-2

FIGURE 6A

Enzyme source:

NG8 A32-2 Marker



Peptidoglycan source: Actinobacillus actinomycetemcomitans 29522

FIGURE 6B

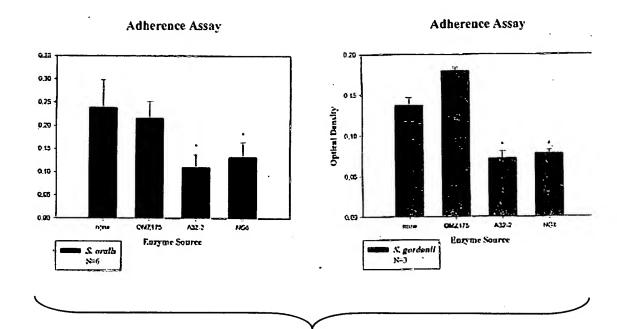


FIGURE 6C

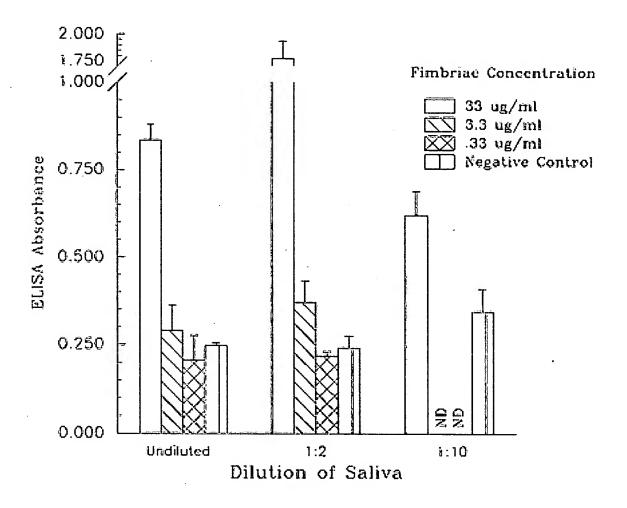
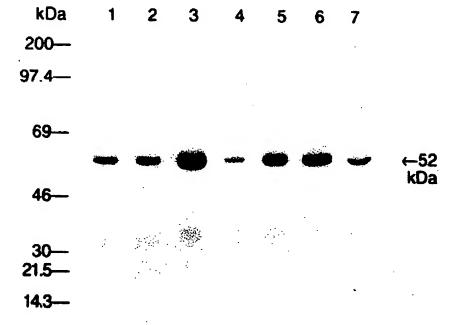


FIGURE 7



kDa 200— 97.4— 69— 46— ←52 kDa

21.5—

14.3—

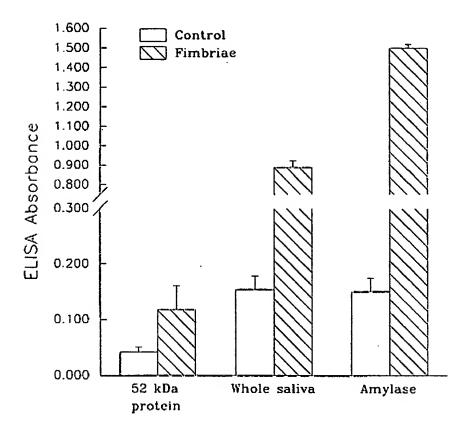
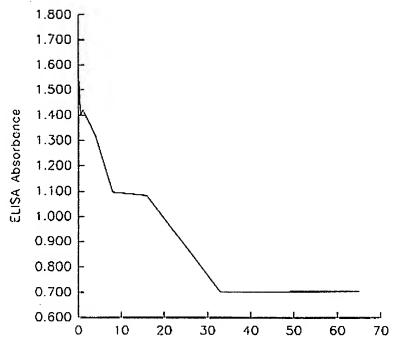


FIGURE 10



Concentration of neutralizing 52 kDa salivary protein ( $\mu g/ml$ )

FIGURE 11

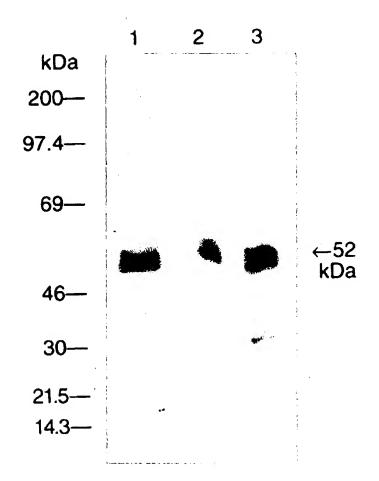


FIGURE 12